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Title:
Perfect score:
                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
   SPTREMBL_16:*
1: sp_archea:*
2: sp_bacteria
3: sp_fungl:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
12: sp_unclass:
13: sp_vertebrs:
14: sp_virus:**
                                                                                                                                                                                                                                                                                                                                                                                                                                        425026 segs, 132305027 residues
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Gapop 10.0 , Gapext 0.5
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4004
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                                                                                   sp_organelle:*
sp_phage:*
                                                                                                                                                                                                            sp_archea:*
sp_bacteria:*
sp_unclassified:*
sp_vertebrate:*
sp_virus:*
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sp_rodent:*
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sp_mhc:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	8	7	6	ر ت	4	ω	2		Result No.
1452.5	1457.5	1458.5	1464	1465.5	1467	1467	1636.5	1644.5	1648.5	1651.5	1652	1652	3028.5	3041.5	3051.5	3159	3945	4004	Score
36.3	36.4	36.4	36.6	36.6	36.6	. 36.6	40.9	41.1	41.2	41.2	41.3	41:3	75.6	76.0	76.2	78.9	98.5	100.0	Query Match Length
871	871	871	871	871	871	852	839	839	839	839	838	838	762	761	761	756	764	764	ength DB
11	11	11	4	11	4	13	4	4	4	4	11	11	11	11	11	11	4	4	æ
Q9EQZ4	Q9EPK8	Q9ES76	Q9HBA0	Q9ERZ8	Q9НВС0	Q9DFS3	Q9NY22	Q9NQ74	Q9н0G9	Q9Н304	Q9JM57	035433	Q9JMI8	8HYQ6D	Q9WUD2	Q9WTR1	Q9Y670	Q9Y5S1	ID
mus		. Q9es76 mus musculu	Q9hba0 homo sapien	Q9erz8 rattus norv	Q9hbc0 homo sapien	Q9dfs3 gallus gall	Q9ny22 homo sapien	Q9nq74 homo sapien		Q9h304 homo sapien		rattus	rattus		Q9wud2 rattus norv	Q9wtrl mus musculu		Q9y5s1 homo sapien	Description

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92009	P79100	Q9VMR4	Q9WOT5	Q9GRV5	Q22374	Q9W3W0	017469	P90784	061220	Q9VUD5	091110	Q9N3Y9	Q9NQA5	Q9JJL2	Q9XSM3	Q9JIP0	Q9R186	Q9H1D0	Q9н1D1	Q9н296	Q9JLM0	Q9н303	Q9Z182	Q9JM56	Q9ERZ7
Q9quq9 mus musculu	P79100 bos taurus	Q9vmr4 drosophila	Q9w0t5 drosophila	Q9grv5 caenorhabdi	Q22374 caenorhabdi	Q9w3w0 drosophila	. 017469 caenorhabdi		061220 caenorhabdi	Q9vud5 drosophila	Q9jjj0 mus musculu	Q9n3y9 caenorhabdi	Q9nqa5 homo sapien	Q9jjl2 rattus norv	Q9xsm3 oryctolagus	Q9jip0 rattus norv	Q9r186 rattus norv	09h1d0 homo sapien	Q9hldl homo sapien	Q9h296 homo sapien	Q9jlm0 rattus norv	Q9h303 homo sapien	Q9z182 rattus norv	Q9jm56 rattus norv	Q9erz7 mus musculu

ALIGNMENTS

	Qy 61 RKGTGASQPDPNRFDRDRLFNAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCL 120	
	QY 1 MTSPSSSPVFRLETLDGGOEDGSEADRGKLDFGSGLPPMESQFQGEDRKFAPQIRVNLNY 60	п о
0;	Query Match 100.0%; Score 4004; DB 4; Length 764; Best Local Similarity 100.0%; Pred. No. 0; Matches 764; Conservative 0; Mismatches 0; Indels 0; Gaps	
	SQ SEQUENCE 764 AA; 85980 MW; A73E3696E70F91E9 CRC64;	70.7
	DR PROSITE; PS50088; ANK_REPEAT; 1. DR PROSITE; PS50297; ANK_REP_REGION; 1.	
	InterPro; IPR002110;	
		-
	RT "A capsaicin-receptor homologue with a high threshold for noxious RT heat.";	
	Caterina M.J., Rosen T.A., Tominaga M.,	. Here
	RP SEQUENCE FROM N.A. RX MEDLINE=99215558; PubMed=10201375;	H H
	OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. OX NCBI_TaxID=9606;	
	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	~
	GN VRL-1.	~ ^
	VANILLOID RECEPTOR-LIKE PRO	
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"ANILLOID RECEPTOR-LIKE PF
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Homo sapiens (Human)
Eukaryota; Metazoa; (
Eukaryota; Eutheria; I
Mammalia; Eutheria; I
NCBI_TaxID=9606;
[1]
                             Pfam; PF00023; ank; 3
PROSITE; PS50088; ANK
PROSITE; PS50297; ANK
SMART; SM00248; ANK;
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Garcia R.L., De
"Cloning and fi
Receptor.
                                                                                                 gene.";
Submitted (NOV-1998) to the
EMBL; AF103906; AAD41724.1;
InterPro; IPR002110; -.
InterPro; IPR002111; -.
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ltheria; Primates;
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Q9WTR1;
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01-NOV-1999 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
GROWTH FACTOR REGULATED C.
VRL1 OR GRC.
Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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    Chordata;
Rodentia;
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Pred.
     Craniata; Ver
Sciurognathi;
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No. 0;
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            Vertebrata;
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P SEQUENCE FROM N.A.
P SEQUENCE FROM N.A.
C STRAIN-C57 BLACK-6; TISSUE-SPLEEN;
EXTRAIN-C57 BLACK-6; TISSUE-SPLEEN;
EXAMAIN-C57 BLACK-6; TISSUE-SPLEEN;
EXAMIN-C57 BLACK-6; TISSUE-SPLEEN;
EXAMIN-C57 BLACK-6; TISSUE-SPLEEN;
EXAMIN-C57 BLACK-6; TISSUE-SPLEEN;
EXBL; ABO2165; BAA78-B78-1; --
R MGD; MGI:1341836; Vrl1.
R INTERPO; IPRO02111; --
R INTERPO; IPRO02111; --
R PIGNITE; PS50088; ANK, REPEAT; 1.
R PROSITE; PS50088; ANK, REPEAT; 1.
R PROSITE; PS50088; ANK, REPEAT; 1.
R PROSITE; PS50088; ANK, REPEAT; 1.
SMART; SM00248; ANK; 1.
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                                                                                  LLVENGANVHARACGREFQKGQGTCFYFGELPLSLAACTKQWDVVSYLLENPHQPASLQA
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                                                   WKLQKAISVLEMENGYWWCRKKQ-RAGVMLTVGTKPDGSPDERWCFRVEEVNWASWEQTL
                                                                                                                            LIYLVFLFGFAVALVSLSQEAWRPEAPTGPNATESVQPMEGQEDEGNGAQYRGILEASLE
                                                                                                                                                                                   LTVVSQVLCFLAIEWYLPLLVSALVLGWLNLLYYTRGFQHTGIYSVMIQKVILRDLLRFL 539
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PTLSEDPSGAGITGYKKNPT---
                     PTLCEDPSGAGVPRTLENPVLASPPKEDEDGASEENYVPVQLLQSN
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                                                                                                                                                                        LTVLSQVLRFVETEWYLPLLVSSLVLGWLNLLYYTRGFQHTGIYSVMIQKVILRDLLRFL
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Pred. No. 7.2e
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 SKPGKNSASEEDHLPLQVLQSH
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Best Local Similarity
Matches 598; Conserv
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Q9WUD2;
Q9WUD2;
01-NOV-1999 (TrEMBLrel. 1:
01-NOV-1999 (TrEMBLrel. 1:
01-MAR-2001 (TrEMBLrel. 1:
VANILLOID RECEPTOR-LIKE P)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor.
SEQUENCE
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Mammalia; Eutheria; Rodentia;
NCBL_TaxID=10116;
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Interpro; IPR002111;
Pfam; PF00023; ank; 3
PROSITE; PS50088; ANK_REPEAT; 1.
PROSITE; PS50297; ANK_REP_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99215558; PubMed=10201375;
Caterina M.J., Rosen T.A., Tominaga M.,
"A capsaicin-receptor homologue with a !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00248; ANK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 398:436-441(1999).
EMBL; AF129113; AAD26364.1;
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ASLQATDSQGNTVLHALVMISDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDL
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77.7%;
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. 12, Last sequence upo
. 16, Last annotation of E PROTEIN 1.
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Pred. No. 2.2
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Sciurognathi; Muridae;
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2e-232;
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Best Local (
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01-MAY-2000 (TrEMBLrel. 13, Last sequence up.
01-MAR-2001 (TrEMBLrel. 16, Last annotation.
STRETCH ACTIVATED CHANNEL 2B.
RSACZB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ishibashi K.;
"Molecular cloning of a stretch activated channel from rat kidney.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AM029330; BAA88637.1; -.
Interpro; IPR002110; -.
Interpro; IPR002111; -.
Interpro; IPR002111; -.
Pfam; PF00023; ank; 3.
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PROSITE; PS50297; ANK_REP_REGION;
SMART; SM00248; ANK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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                       TPLKLAAKEGKIEIFRHILQREFSG-LSHLSRKFTEWCYGPVRVSLYDLASVDSCEENSV
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                                                                                                                                                                                                                                                                                                                                                          MTSPSSSPVFRLETLDGGQEDGSEADRGKLDFGSGLPPMESQFQGEDRKFAPQIRVNLNY 60
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                                                                                                                                                                                                   LQCVKLLVENGANVHARACGRFFQKGQGTCFYFGELPLSLAACTKQWDVVSYLLENPHQP
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77.5%;
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Pred. No. 1.4e-231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8977CDE1D5351EC8 CRC64;
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                                                                                                                          Query Match
Best Local Similarity
Matches 594; Conser
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Q9JMI8;
01-OCT-2000 (TIEMBLIEL 1
01-OCT-2000 (TIEMBLIEL 1
01-MAR-2001 (TIEMBLIEL 1
                                                                                                                                                                        Pfam; PF00023; ank; 3.

PROSITE; PS50088; ANK_REPEAT; 1.

PROSITE; PS50297; ANK_REP_REGION;
SMART; SM00248; ANK; 1.

SEQUENCE 762 AA; 86767 MW; CE
                                                                                                                                                                                                                              Submitted (JAN-1999) to the EMBL; AB022332; BAA93435.1; Interpro; IPR002110; -. Interpro; IPR002111; -.
                                                                                                                                                                                                                                                                                   Suzuki M.;
                                                                                                                                                                                                                                                                                              TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                     ION CHANNEL
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GKTCLMKAVLNLQDGVNACIMPLLQIDKDSGNPKLLVNAQCTDEFYQGHSALHIAIEKRS
                                       MTSASSPPAFRLETSDGDEEGNAEVNKGKQE----PPPMESPFQREDRNSSPQIKVNLNF
                                                                                            MTSPSSSPVFRLETLDGGQEDGSEADRGKLDFGSGLPPMESQFQGEDRKFAPQIRVNLNY
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                                                                                                                           Conservative
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oa; Chordata;
ia; Rodentia;
                                                                                                                                                                             86767 MW; CE0970BC4195351E
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77.4%;
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Last annotation update)
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                                                                                                                         Score 3028.5; DB 11
Pred. No. 1.5e-230;
2; Mismatches 94;
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                                                                                                                                                                                                                                                                                                                                                                                                                        762
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Query
Best I
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                                                                                                                                                                           Rattus norvegicus (Rat).
Rattus norvegicus (Chordata;
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                       PROSITE; PS50088; ANK_REPEAT; 1. PROSITE; PS50297; ANK_REP_REGION; SMART; SM00248; ANK; 1.
                                                                                        pathway.";
Nature 389:816-824(1997).
EMBL; AF029310; AAC53398.1;
                                                                                                                                  Caterina M.J.,
                                                                                                                                            MEDLINE=98007969; PubMed=9349813;
                                                                                                                                                                  NCBI_TaxID=10116;
                                 SEQUENCE
                                                                 Pfam; PF00023;
                                                                         InterPro; IPR002110;
InterPro; IPR002111;
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Local Similarity
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Pred.
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Sciurognathi;
                                 DAFC80B12BDF71BF
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1652; DB 1
No. 8e-122;
                                                                                                                                                                                      Vertebrata;
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Q9JM57;
Q1-OCT-2000 (
01-OCT-2000 (
01-MAR-2001 (
SEQUENCE FROM N.A.
Tsutsumi S., Nakamura A.,
"Vanilloid receptor type
Submitted (MAR-2000) to t
                                                                                                                                                                                 VR1L1.
Rattus norvegicus (Rat).
                                                                                                                                         Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                           VANILLOID RECEPTOR
                                                                                                                   NCBI_TaxID=10116
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(TremBLrel. 15, Last sequence update)
(TremBLrel. 16, Last annotation updat
ECEPTOR TYPE 1 LIKE PROTEIN 1.
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like protein 1.";
e EMBL/GenBank/DDBJ
                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Best Local
Q9H304 PRELIMINARY;
Q9H304;
Q1-MAR-2001 (TrEMBLrel. 16,
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PROSITE; PS50297; ANK_REP_REGION;
SMART; SM00248; ANK; 1.
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InterPro; IPR002111;
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                                                                                                                                   VNKIAQESKNIWKLQRAITILDTEKSFLKCMRKAFRSGKLLQVGFTPDGKDDYRWCFRVD
                                                                                                                                               VNSVATDSWSIWKLQKAISVLEMENGYWWC-RKKQRAGVWLTVGTKPDGSPDERWCFRVE
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                                                                                                                                                                                                                               LCRFMFVYLVFLFGFSTAVVTLIED-----GKN---NSLPMESTPHKCRGSACKPGN
                                                                                                                                                                                                                                                    LLRFLLIYLVFLFGFAVALVSLSQEAWRPEAPTGPNATESVQPMEGQEDEGNGA-----
                                                                                                                                                                                                                                                                           FVQSLFMLVSVVLYFSQRKEYVASMVFSLAMGWTNMLYYTRGFQQMGIYAVMIEKMILRD
                                                                                                                                                                                                                                                                                                                        -EGLPPYKLKNTVGDYFRVTGEILSVSGGVYFFFRGIQYFLQRRPSLKSLFVDSYSEILF
                                                                                                                                                                                                                                                                                                                                    AAKEGKIEIFRHILQREF--SGLSHLSRKFTEWCYGPVRVSLYDLASVDSCEENSVLEII 358
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46.3%; Pred. No. 8e-122;
ative 127; Mismatches 230;
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Best Local Sim
Matches 344;
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SEQUENCE
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CONTITION D., Peck A., Zou T.;

CONTITION D., Peck A., Zou T.;

"Cloning and characterization of the human capsaicin receptor, submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF196175; AAG43466.1; -.
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01-MAR-2001 (TrEMBLrel.
CAPSAICIN RECEPTOR.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                              GFAVALVSLSQEA-------WRPEAPTGPNATESVQPMEGQEDEGNGAQYRGIL
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                                                     WNTNVGIINEDPGNCEGVKRTLSFSLRSS
                                                                                                          ESKNIWKLQRAITILDTEKSFLKCMRKAFRSGKLLQVGYTPDGKDDYRWCFRVDEVNWTT
                                                                                                                                                             STCLELFKFTIGMGDLEFTENYDFKAVFIILLAYVILTYILLLNMLIALMGETVNKIAQ
                                                                                                                                                                                                               GFSTAVVTLIEDGKNDSLPSESTSHRWRGPACRPPDSS-----
                                                                                                                                                                                                                                                                                                                      GDYFRVTGEILSVLGGVYFFFRGIQYFLQRRPSMKTLFVDSYSEMLFFLQSLFMLATVVL
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Last annotation updat
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Pred. No. 8.8e-122;
2; Mismatches 199;
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.8e-122;
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01-MAR-2001 (
01-MAR-2001 (
HYPOTHETICAL
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Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases EMBL; AL136801; CAB66735.1;
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                        GFAVALVSLSQEA------
                                                                                                                                                                      CGRFFQKGQG-TCFYFGELPLSLAACTKQWDVVSYLLENPHQPASLQATDSQGNTVLHAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FDRDRLENAVSRGVPEDLAGLPEYLSKTSKYLTDSEYTEGSTGKTCLMKAVLNLKDGVNA 133
WNTNVGIINEDPGNCEGVKRTLSFSLRSS----RVSGRHWKNFALVPLLR
                  WEQTLPTLCEDPSGA-GVPRTLENPVLASPPKEDEDGASEENYVPVQLLQ
                                                                                  STCLELFKFTIGMGDLEFTENYDFKAVFIILLLAYVILTYILLLNMLIALMGETVNKIAQ
                                                                                              EASLELFKFTIGMGELAFQEQLHFRGMVLLLLLAYVLLTYILLLNMLIALMSETVNSVAT
                                                                                                                           GFSTAVVTLIEDGKNDSLPSESTSHRWRGPACRPPDSS------
                                                                                                                                                                                                                  GDYFRVTGEILSVLGGVYFFFRGIQYFLQRRPSMKTLFVDSYSEMLFFLQSLFMLATVVL
                                                                                                                                                                                                                               GNSMLLTGHILLLGGIYLLVGQLWYFWRRHVFIWISFIDSYFEILFLFQALLTVVSQVL
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
194.9 KDA PROTEIN.
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                                                                                                                                               -WRPEAPTGPNATESVQPMEGQEDEGNGAQYRGIL
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RESULT
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Best Local Similarity 48.5%;
Matches 344; Conservative 121
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Q9NQ74;
Q1-OCT-2000 (TrEMBLrel. i)
O1-OCT-2000 (TrEMBLrel. i)
O1-MAR-2001 (TrEMBLrel. i)
VANILLOID RECEPTOR 1.
VR1.
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"Cloning and functional expression of a human orthologue of rat vanilloid receptor-1." submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR002111; -.
Pfam; PF00023; ank; 3.
PROSITE: PS50088; ANK_REPEAT; 1.
PROSITE: PS50297; ANK_REP_REGION;
SMART; SM00248; ANK; 1.
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Mammalia; Eutheria;
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Metazoa; Chordata; C
~~+heria; Primates; (
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58; Pred. No. 3.1e-121;
121; Mismatches 200;
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Catarrhini; Hominidae;
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PROSITE; PS50088; ANK_REPEAT; 1.
PROSITE; PS50297; ANK_REP_REGION;
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InterPro; IPR002111; -
InterPro; IPR002111; -
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Weerasekera N., Rang H., Savidge
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TISSUE=DORSAL ROOT GANGLION;
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                      ILQREFS--GLSHLSRKFTEWCYGPVRVSLYDLASVDSCEENSVLEIIAF-HCKSPHRHR
                                                             VEVADNTADNTKFVTSMYNEILILGAKLHPTLKLEELTNKKGMMPLALAAGTGKIGVLAY
                                                                                                     VMISDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKLAAKEGKIEIFRH
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Pred. No. 1.3
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Best Local
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O9DES3; O1-MAR-2001 (TIEMBLIEL 16,
01-MAR-2001 (TIEMBLIEL 16,
01-MAR-2001 (TIEMBLIEL 16,
                                                                                                                                                                                                                                                                         Liedtke W., Choe Y., Marti-Renom M.A., B
Hudspeth A.J., Friedman J.M., Heller S.;
"Vanilloid Receptor-Related Osmotically
Candidate Vertebrate Osmoreceptor.";
Cell 103:525-535(2000).
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
VANILLOID RECEPTOR-RELATED OSMOTICALLY ACTIVATED CHANNEL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
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                                                                                                                                                                                                                                                Receptor
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                EYLSKTSKYLTDSEYTEGSTGKTCLMKAVLNLKDGVNACILPLLQIDRDSGNPQPLVNAQ
                                           GTYRQHPSENKRWRRRVVEKPVAGTKGPAPNPPPVLKVFNRPILFDIVSRGSPDGLEGLL
                                                                                                  AEPSRGPPGAGDGKQNLRMKFHGAFRKGPPKPMELLESTIYESSVVPAPKKAPMDSLFDY
                                                                                                                             SEADRGKLDFGSGLPPMESQFQGEDRKFAPQIRVNL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WNTNVGIINEDPGNCEGVKRTLSFSLRSS----RVSGRHWKNFALVPLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WEQTLPTLCEDPSGA-GVPRTLENPVLASPPKEDEDGASEENYVPVQLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSWSIWKLQKAISVLEMENGYWWC-RKKQRAGVMLTVGTKPDGSPDERWCFRVEEVNWAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STCLELFKFTIGMGDLEFTENYDFKAVFIILLLAYVILTYILLLNMLIALMGETVNKIAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GFAVALVSLSQEA-------WRPEAPTGPNATESVQPMEGQEDEGNGAQYRGIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDYFRVTGEILSVLGGVYFFFRGIQYFLQKRPSMKTLFVDSYSEMLFFLQSLFMLATVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MLLVEPLNRLLQDKWDRFVKRIFYFNFLVYCLYMIIFTMAAYYRPV---DGLPPFKMEKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESKNIWKLQRAITILDTEKSFLKCMRKAFRSGKLLQVGYTPDGKDDYRWCFRVDEVNWTT
                                                                                                                                                         al Similarity
338; Conser
                                                                                                                                                                                                                                                             AF261883; AAG28026.1;
                                                                                                                                                                                                                                  852 AA;
                                                                                                                                                            Conservative
Neognathae;
                                                                                                                                                                         36.6%;
41.7%;
                                                                                                                                                                                                                                  96197 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                           121;
                                                                    ---GTGASQPDP----NRFDRDRLFNAVSRGVPEDLAGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                        Score 1467;
Pred. No. 3.
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                                                                                                                                                            Mismatches
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                                                                                                                                                                       ; DB 13;
3.3e-107;
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16;

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RESULT
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  Query Match
Best Local
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Q9HBC0;
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
OTRPC4.
                                                                                      SEQUENCE
                                                                                                             "OTRPC4, a nonselective cation clearity.";
extracellular osmolarity.";
Nat. Cell Biol. 2:665-702(2000).
EMBL; AF258465; AAG16127.1; -.
                                                                                                                                                                            PubMed=11025659;
Strotmann R., Harteneck C., Nunnenmacher K.,
"OTRPC4, a nonselective cation channel that of
                                                                                                                                                                                                                                              SEQUENCE FROM N.A. TISSUE-RENAL CORTEX;
                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRAFRSGEMVTVGKGTDGTPDRRWCFRVDEVNWSHWNQNLGIISEDPGKSDTYQYYGFSH
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  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----VPRTLENPVLASPPKED 746
                                                                                        871 AA;
                                                                                      98294 MW;
  36.6%;
43.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                          16,
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Last sequence update)
Last annotation update)
Score
Pred.
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                                                                                        C62056B86DEA6FB6
1467; DB 4;
No. 3.4e-107;
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                     Length
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                       871;
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Q9ERZ8;
Q1-MAR-2001
01-MAR-2001
01-MAR-2001
        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                         VROAC.
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                                                                                                                                                                                                                                                                                                                                                      AVALVSL-----SQEAWRPEAPTGPNATESVQPMEGQEDEGNGAQYRGILEASLE
                                                                                                                                                                                                                                                                                                                                                                                                MLLTGHILILLGGIYLLVGQLW-YFWRRHVFIWISFIDSYFEILFLFQALLTVVSQVLCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLEPLNKLLQAKWDLL-IPKFFLNFLCNLIYMFIFTAVAYHQPTLKKQAAPHLKAEVGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QREFS--GLSHLSRKFTEWCYGPVRVSLYDLASVDSC-EENSVLEIIAFHCKSPHRHRMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISDNSAENIALVTSMYDGLLQAGARLCPTVQLEDIRNLQDLTPLKLAAKEGKIEIFRHIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RFFQ-KGQGTCFYFGELPLSLAACTKQWDVVSYLLENPHQPASLQATDSQGNTVLHALVM
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                                                                                                                                                                                                                                         WKLQWATTILDIERSFPVFLRKAFRSGEMVTVGKSSDGTPDRRWCFRVDEVNWSHWNQNL
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D RECEPTOR-RELATED 0
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                                                                  , Last sequence update)
, Last annotation update)
OSMOTICALLY ACTIVATED CH
                                                                                                        Created)
                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor.
SEQUENCE
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PubMed-11081638;

Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,

Sali A., Hudspeth A.J., Friedman J.M., Heller S.;

"Vanilloid receptor-related osmotically activated channel (VR-OAC),

candidate vertebrate osmoreceptor.";

Cell 103:525-535(2000).
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793 GIINEDPGKSEIYQYYGFSHTMGRLRRDRWSSVVPRVVE-----LNKNSGTDEVVV 843
                          719 PTLCEDPS----
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                                               ASALVTLLNPCTNMKVCNEDQSNCTVPSYPACRDS-----
                                                                                                                                                                                                     RFFQ-KGQGTCFYFGELPLSLAACTKQWDVVSYLLENPHQPASLQATDSQGNTVLHALVM 254
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                                                                                                                                                                              AVALVSL-----SQEAWRPEAPTGPNATESVQPMEGQEDEGNGAQYRGILEASLE 599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          871 AA; 98009 MW;
                      -----GAGVPRTLENPVLASPPKEDEDGASEENYV 756
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Oy 757 PVQLL 761 |: | Db 844 PLDNL 848

Search completed: July 18, 2001, 16:00:08 Job time: 136 sec